The Longitudinal Effects of Supplemental Forage on Honey Bee Colony Growth, Immunity, and Pathogen Resistance

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Objectives

Determine effects of supplemental forage on honey bee health

1) Pathogen load
2) Immune system function
3) Rapini cover crop versus native plant mix

Methods

- 32 experimental colonies
- 16 almond orchards in the Central Valley
  - –4 with rapini flower plot
  - –4 with mixed native flower plots
  - –8 control plots without flowers
- Sampling points
- Monthly samples from December until June
- Methods
  - 16S rRNA gene survey of the gut microbiome
  - PCR and quantitative PCR screening of pathogens
  - Quantative PCR of immune genes

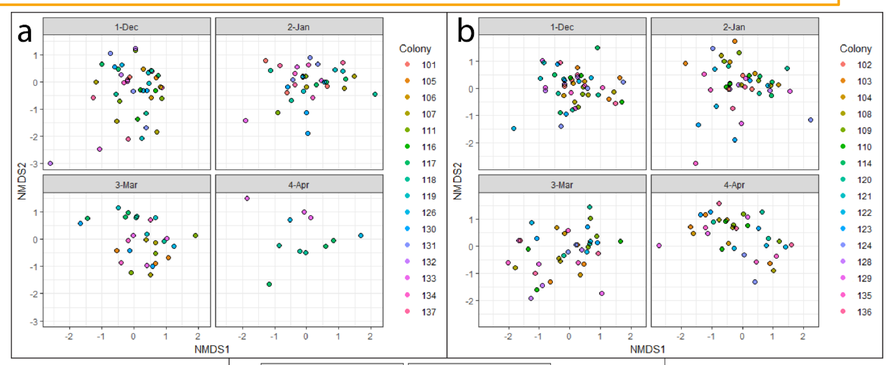
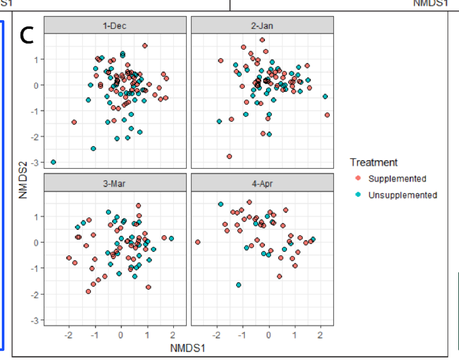


Fig 1 : a) Foragers that did not receive supplemental forage, b) Foragers that received supplemental and c) Individual foragers grouped by forage treatment by timepoint. The only significant differences between the microbiota of supplemented and non-supplemented bees occurred during the March timepoint (*P*=0.042).



Results

Pathogen screens and immune system function ongoing. For Colony Health see 17POLL20 Niño. Gut microbe analyses are reported here.

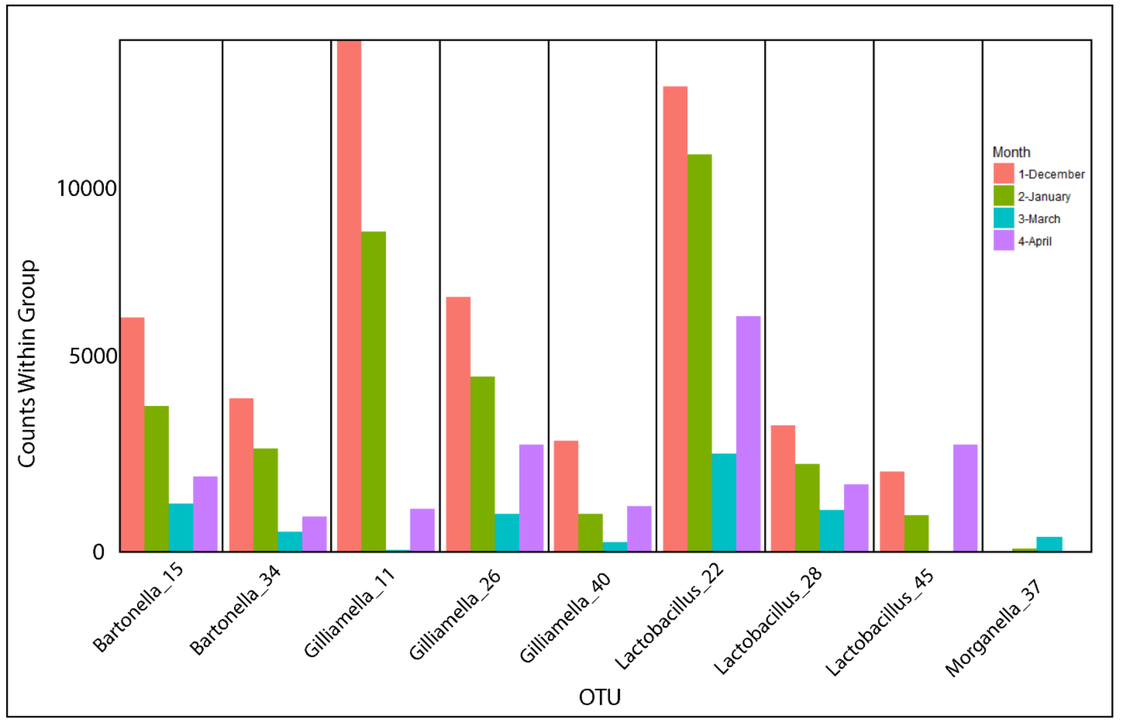


Fig 2 Counts within group of the differentially abundant bacterial taxa binned by the sampling time point within forage-treated bees. Only March had a significantly decreased proportional abundance of OTUs as compared to the initial December timepoint. (*Padj.* <0.05).

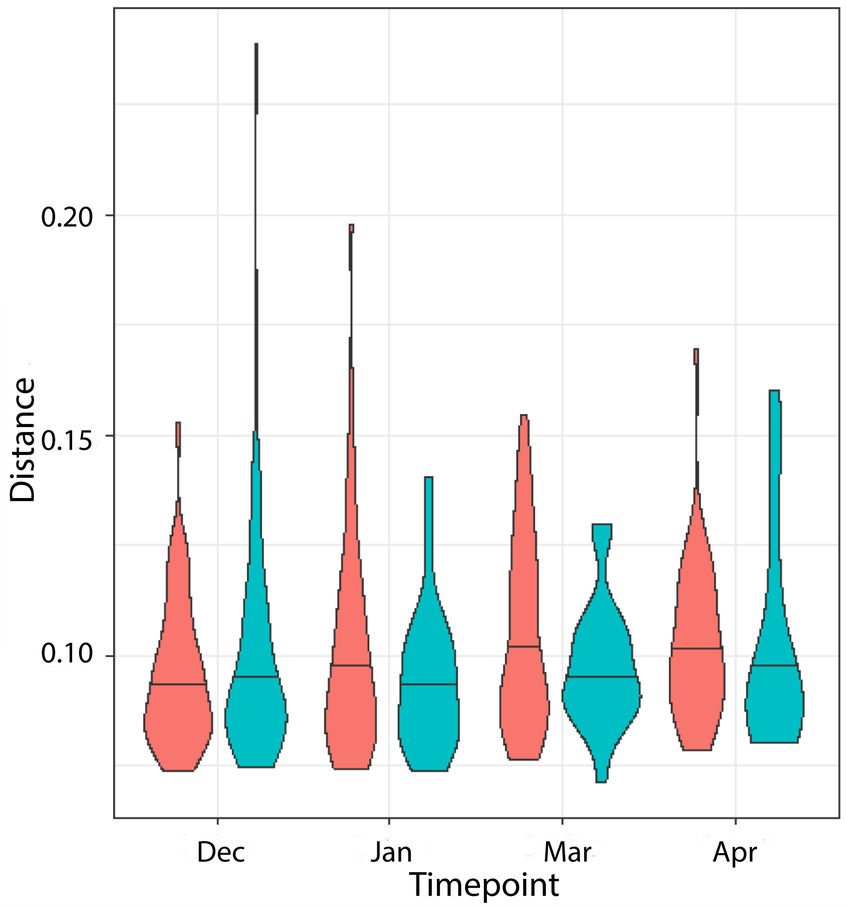


Fig 3. Violin plot of the weighted UniFrac distances between forage-supplemented and non-supplemented bees at all timepoints. The bee gut microbiome changes slightly over time, with forage-supplemented bees having significantly different microbiomes in both the January (F=2.28, R^2=0.03, P=0.041), and March (F=2.39, R^2=0.04, P=0.042) time points

CONCLUSIONS

- Honey bee gut microbes are incredibly resilient to diet treatment
  - –Supplemental forage had only small effects on gut microbial community
  - –Important for bee health
- Abundance of specific microbes varied across forage treatment and season
- Gut microbial communities vary as much within a colony as between different colonies

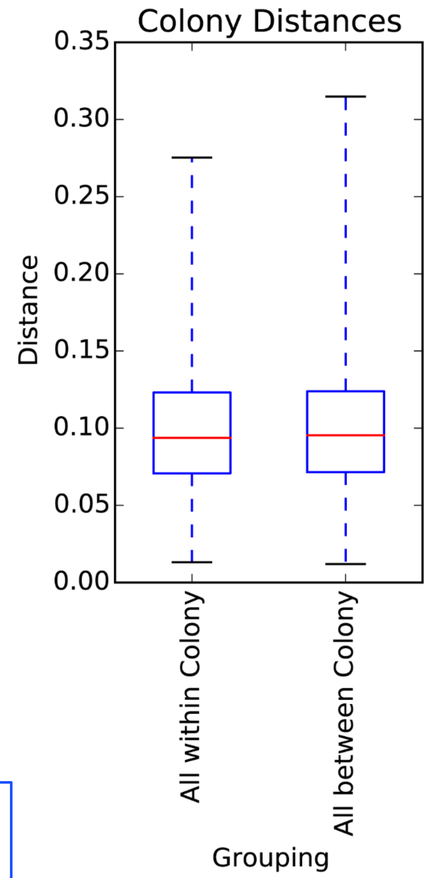


Fig 4. Box and whisker plots of the weighted UniFrac distances of forager microbiomes within the same colony of origin versus all colonies together across all timepoints. There is no significant difference between the gut communities of colony mates and foragers of separate colonies (t= -1.80, P=0.075).

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